

SEQUENCE LISTING

<110> Ballance, David J.
Sleep, Darrell
Turner, Andrew J.
Sadeghi, Homa
Prior, Christopher P.

<120> Albumin Fusion Proteins

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<170> PatentIn Ver. 2.1

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 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat		384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His		
115	120	125
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga		432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg		
130	135	140
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg		480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg		
145	150	155
160		
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc		528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala		
165	170	175
tgc ctg ttg cca aag ctc gat gaa ctt cggt gat gaa ggg aag gct tcg		576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser		
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tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa		624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu		
195	200	205
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc		672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro		
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aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa		720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys		
225	230	235
240		
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac		768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp		
245	250	255
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc		816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser		
260	265	270
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac		864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His		
275	280	285
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca		912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser		
290	295	300
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct		960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala		
305	310	315
320		
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga		1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg		
325	330	335
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca		1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr		
340	345	350

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa		1104	
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Asp Pro His Glu			
355	360	365	
tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct		1152	
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro			
370	375	380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag		1200	
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu			
385	390	395	400
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc		1248	
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro			
405	410	415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa		1296	
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys			
420	425	430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt		1344	
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys			
435	440	445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat		1392	
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His			
450	455	460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc		1440	
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser			
465	470	475	480
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca		1488	
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr			
485	490	495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat		1536	
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp			
500	505	510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca		1584	
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala			
515	520	525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg		1632	
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu			
530	535	540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag		1680	
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys			
545	550	555	560
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt		1728	
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val			
565	570	575	
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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Tyr Leu Tyr Glu Ile Ala Arg
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Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
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Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
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Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
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Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
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Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
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Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
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Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
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Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
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Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
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Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
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Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

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Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
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Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
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Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
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Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
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Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
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Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
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fusion protein in which the albumin moiety is c-terminal of
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<221> misc_feature
<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactttgt gtgcacnnnn nnnnnnnnnn nn 52

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg
20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI restriction site

<220>
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<222> (11)..(16)
<223> Hind III restriction site

<220>
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<222> (17)..(27)
<223> Kozak sequence

<220>
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<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tggtaacct ttatttcct tcttttctc 60
tttagctcggtt cttactcgag gggtgtgttt cgtcgagatg cacacaagag tgag 114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
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<222> (6)..(11)
<223> Asp718 restriction site

<220>
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<222> (12)..(17)
<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31

gcagcggtac cgaattcggc gcgccttata agcctaaggc agc

43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic protein into pC4:HSA vector

<220>
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<220>
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<221> misc_feature
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<220>
<221> misc_feature
<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccggccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn 46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic protein into pC4:HSA vector

<220>
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<222> (38)
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<220>
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<220>
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<223> n equals a,t,g, or c

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<222> (45)
<223> n equals a,t,g, or c

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<222> (46)
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<221> misc_feature
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<223> n equals a,t,g, or c

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<222> (52)
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<220>
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<222> (53)
<223> n equals a,t,g, or c

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<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactttgt gtgcacnnnn nnnnnnnnnn nnnnn 55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser
1 5 10 15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20

<210> 36

<211> 66
<212> PRT
<213> Agkistrodon piscivorus

<400> 36
Ile Thr Tyr Thr Asp Cys Thr Glu Ser Gly Gln Asn Leu Cys Leu Cys
1 5 10 15

Glu Gly Ser Asn Val Cys Gly Lys Gly Asn Lys Cys Ile Leu Gly Ser
20 25 30

Gln Gly Lys Asp Asn Gln Cys Val Thr Gly Glu Gly Thr Pro Lys Pro
35 40 45

Gln Ser His Asn Gln Gly Asp Phe Glu Pro Ile Pro Glu Asp Ala Tyr
50 55 60

Asp Glu
65

<210> 37
<211> 71
<212> PRT
<213> Agkistrodon piscivorus

<400> 37
Glu Ala Gly Glu Glu Cys Asp Cys Gly Ser Pro Glu Asn Pro Cys Cys
1 5 10 15

Asp Ala Ala Thr Cys Lys Leu Arg Pro Gly Ala Gln Cys Ala Glu Gly
20 25 30

Leu Cys Cys Asp Gln Cys Lys Phe Met Lys Glu Gly Thr Val Cys Arg
35 40 45

Ala Arg Gly Asp Asp Val Asn Asp Tyr Cys Asn Gly Ile Ser Ala Gly
50 55 60

Cys Pro Arg Asn Pro Phe His
65 70